GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nuc	OM nucleic - nucleic search, using sw model
Run on:	April 13, 2003, 02:11:28 ; Search time 129.415 Seconds (Without alignments) 3373.191 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-813-990A-1_COPY_441_455 15 1 99tttegttletect 15
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched:	2054640 segs, 14551402878 residues
Total number of	Total number of hits satisfying chosen parameters: 4139280
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ALIGNMENTS

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RESOLT 1 RED44387 LOCUS DEFINITION	ACCESSION VERSION KEYWORDS	SOURCE ORGANISM	REFERENCE AUTHORS TITLE

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DITACID PTEDVGGULPHRIESYMGYTLTTGFEEGFRÄGERATGAPKYM. KGAVVV
PKPEKDSAKENQPHRIMANEANSGIGSYFGGSLLSVDINGEHIDDLATGAPLYSGVTH
DESRVYVYSKPGGRTLESWTESSYFFULDEMSLIGGREGOTALASAGELNNIKKNUV
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AGGRSTESVIDLIYVITESGKGSLGEKRLEFRIALSPTSVTTRGOLFIKSKTETGY
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Cloding and characterization of incegrie alpha subcuits from the
solitary ascidian, Halocynthia noretmi
J. Immunol. 166 (3), 1716—1215 (2001)
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100.0%; Pred. No. 9.9e+62:
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Stolidobracchia: Pyuridae; Halocynchia.
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/protein_id="awa21479.1"
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/gene="HrlfGAl"
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gegviyydprconiqhltggivsellysendhviagqvlirldgttiranlstvestl
aqlyarrarlkaerigaesfevbenitdlisstsagki"
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LRDFDQIRFLSGMGPPAMFDLPWLPFYIVTCFLFHPATGYTATGGSLVLATLTFMTN
QGIFTLSKKQSDSANMRNAFAQTSIRNSFVIHAMGMAGTMAEINDRKNSEYRTITRGA
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VSFGLRAGSALGVIGYSASGKSSLARAMGIWPTVRGSTRLDGAALDQWDGDALGRHT
GYLPQDVELFSGTVAQNICRFAKEMSPEVVVAAARAAKVHDLILRLPNGYEFFIGESG
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AHRSGVLAVCDFVLAMQEGRAIAFGPKEEVLARVSRPEAARTPIAERVAQLKVVVJGM
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Halocynthia roretzi HrITGAl mRNA for integrin alpha Hrl, complete
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        whose products are homologues to a family of ATP binding proteins Microbiology 143 (Pt.4), 1389-1394 (1997)
                                                                                                                                                                                       Submitted (29-DEC-1995) Jaroslaw E. Krol, General Microbiology, M.Curie-Sklodowska University, Akademicka 19, Lubiin, 20-033,
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AB048261/c
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TITLE
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/db_xief="SPIPHEMBL:Q52900"
/transletion="MICHEMBRAPHEMBRAYOLVDFLACHVENATKNOYAGSPPH
KTVAPGTSHTREGNOPA:HTBHAACHEMPWKDSYAKSGHTSLAMLIGTDREVVAECP
DTILTELYANDATHEMPROJAGSHTNIGDTHALMGACHGAPLSSAP"

1 1430 - 1553 q 1.127 t
          GLASKKOGTAEJIKGIVVQINATNOSIGIIEBRIGGIDVIYKKGIVTLERRSAGNGTO
BSPGQREGNOSKGSIGGKALIETIRGGIGLINEDRASBIZAKTITOVANGINASTERASE
KSIGGORGASIGNSKAPATNONIVTIRGGILINVENNEITIVENNEITIVENNEITIVENNEITIVENNATATEGILS
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Fleischmann.R.D., Alland.D., Eisen.J.A., Carpenter,D., White,C.,
Peterson.J., DeBoy.K., Dodsch.R., Gwinn.M., Haft.D., Hickey.E.,
Kolonay.J.F., Nolson.W.C., Smayam.L.A., Ermolaeva.M.,
Salzberg.S.L., DeLoher.A., Utterback.I., Neidman.J., Khohri.H.,
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Submitted (25-APR-2001) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, M. 2085u, 95A
Location/Guallifers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis CDC1551
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                                                                                                                                                     KTIKLYPSMPAEVEIKIGDRIVISYLIKELTDQMSHVERQET
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100.0%; Fred. No. 3.96±92;
Live 0: Mishatches
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/protein_id "JAA£6801.1"
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Gill, J., Mikula, A. and Bishai, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref-".axon:83331"
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/gene="MT1018"
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/gene-"MIT018"
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AE006986 AE006516
AE006986.1 GI:13880583
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/denc-"OkF3"
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Rest Local Similarity 160.7
Matches 15, Conservative
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SDVGNGYATLSKIFRIALOSGTLATGAILV10G0ASSGTITAGSILTSRALAAPVEAAI
GNWRGYAROSGARALSSILKTTPEIPAPLALAAPTKOVTVEGIASGPPAGGRLV1SD
VSFGLRAGSALGVIGY-SASGKSSLARAMGIMPTVKGSIREDGAALDOMODALGRHT
GYLPQDYVELFSGTVAONTCRFAKEMSFEVVVAAARARHUBLIIRLPNGYEFIGEG
AALSAGORORIALARALYGEPFLVVLDEPNSNLDEEGERALSAAIMSVRARGGTVVVI
AHRSGYLAVCDFVLAMQEGRMIAFGEKEVLARVSRPEAARTPILARALAGGLKVVVDGM
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LRDFDQIRTFLSGMGPTAMFDLPWLPFYIVICFLFHPAIGYIAIGGSLVLAILTFMIN
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/translation-"MSKVISESKRSLNKHVAVVGVLSIALVCGIGGWAATTELSSAVI
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On Jan 29, 1997 this sequence version replaced gi:1360123.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identification of genes in Rhizobium legaminosarum bv. tritolist whose products are homologues to a family of ATP-binding proteins Microbiology 143 (Pt 4), 1389-1394 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group:
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                           Rhizobium leguminosarum prsD, prsE, ORF3 genes.
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/db_xref="G1:1360124"
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/db_xref+"GI:1360125
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                                                                                                                                                                                                                                              5263 hp
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Rhizobium leguminosarum.
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/clone_lib="pARF136"
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Krol, J. and Skorupska, A.
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/gene="prsD"
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2984. .4285
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Saps

linear PMI 22-001-1995

BASE COUNT

Matches

AK122817/c DEFINITION

RESULT 6

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ACCESSION

KEYWORDS

SOURCE

VERSION

ORGANISM

REFERENCE AUTHORS

TITLE

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H.sapiens CpG island DNA genomic Msel Tragment, clone 88a6, forward
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H.sapiens CpC island DNA genomic Msel fragment, clone 88a6, reverse
read cpq88a6.rtla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vector: pGEM-521(-)
Clones are available from the UK MWC Human Genome Mapping Broject
Resource Centre, Hinxtos, Carbidgeshire CHIS ING, UK. See OHL:
http://www.hgmp.mrc.ac.ik/ for details
                                                                                                                                                                                                                                                                                                                                                                                    Submitted (16 OCT-1995) The Sunger Centre, Hiskton, Cambridgeshirs CBLC 180, England, E mail Doutact: Innequery/Sanger.ac.uk
2 (Asset 1.0 16)
(Cross, San Chaife, Man, Nan, X. and Bird, A.P. Perilication of Cps Island Nan, X. and Bird, A.P. Perilication of Cps Islands using a methylated DNA binding cultumn Nat. Gener. 6 (5), 236-244 (1994)
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Mammalias Butherias Primates: Catarrinis Hominidaes Homos
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Submitted (16-00T-1995) The Sanger Centre, Hinxton, Tambridgeshive
CBPO 1RQ, England E-mail Contact: humquery-dsanier.ac.uk
2 (Dases 1 to 160)
Cross,S.H., Charlton,J.A., Nan,X. and Bird,A.F.
Purlibration of CpG islands using a metnylated DNA Linding column
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Mammalia: Eutheria: Primates: Catarriini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                               1 (bases I to 160)
Maddonald.M., Brokle.E., Wilkinson.P. and Micklem.3.
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160.0%; Pred. No. 1.6e.04;
tive 0: Mismatches 0;
                                                                                                                                   N.S
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                                                                                                                                                                                                           263622.1 GI:1036000
GFG island, genomic Msel fragment.
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/db_xref="taxon:96v6"
/elone="88a6"
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/clone_lib="cor-1"
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| 57 c 48 g
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Best Local Similarity 160.5
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Mammalia; Eutheria; Primates; Catarnini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang,T., Watanabe,Y., Henderson,R.A., Johnson,J.C., Retter,M.W., Marnerakis,M., Carter,D., Fanger,G.R., Vedvick,T.S., Bangur,C.S., Mcnabb,A., Fanger,N., Switzer,A., Mcneill,P.D. and Clapper,J.D. Compositions and methods for the therapy and diagnosis of lung
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 71)
Janjic,N., Gold,L., Schmidt,P. and Vargeese,C.
Vascular endothelial growth factor (VEGF) Nucleic Acid Ligand
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                                                                 Length 51;
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/db_xref="taxon:9606"
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AX368155/C DEFINITION

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RESULT 7

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REFERENCE AUTHORS JOURNAL

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PEATURES

BASE COUNT

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Saps ë

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